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BIOBANKING FOR GLOBAL CHALLENGES

Graduation towers microbiome – biobanking and analyzing data from specific microbial environment

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INTRODUCTION

The biodiversity of microorganisms particularly genetic diversity, is one of the Earth's greatest treasures. Microbiomes of hypersaline environments like graduation towers are still not well known. Thus, more attention regarding heterogeneity investigations should be paid.

AIM

The aim of these study was to present the biodiversity of graduation towers located in Lodz/Poland and the possible influence of the graduation tower environments on the changes in species composition of the brine

METHOD

Samples were collected from three graduation towers located in Lodz/Poland and brine springs from Zablocie/Poland. The brine from Zablocie was used to fill the tested graduation towers. DNAs from samples were isolated and prepared for sequencing according to the 16S Metagenomic Sequencing Library Preparation protocol from Illumina. Libraries were sequenced on Ilumina MiSeq platform in 2x250 bp configuration. Generated data were analyzed with the Qiime2 platform.

RESULTS

During the research, the biodiversity of the studied sites was analyzed. Based on the Bray-Curtis diversity metrics, PCoA (Principal coordinates analysis) was performed (Fig. 1). Clusters for individual sampling locations can be noticed. This suggests the existence of some differences in the level of biodiversity between individual locations, even though the graduation towers are filled with the brine from the same single source - Zablocie.

Significant differences in biodiversity between groups were confirmed by comparing the Shannon index (Fig. 2) and the observed OTU number (Fig. 3). The result of the analysis confirms the statistically significant differences between the samples from the Zablocie and the other groups, and between GT1 and GT2. At the level of the number of observed OTUs (Fig. 3), a statistically significant difference between GT2 and GT3 was also demonstrated.

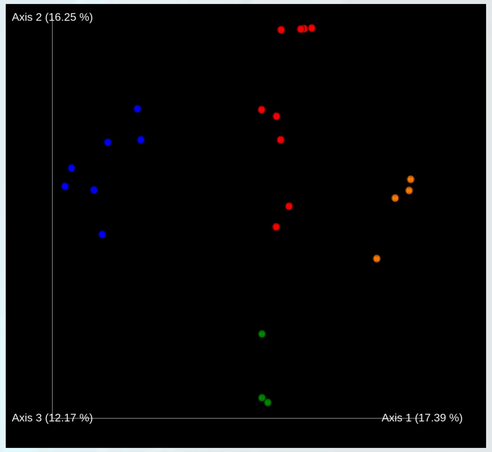


Fig. 1 PCoA Emperor plots based on Bray-Curtis diversity metric. The source of a given sample is marked with colors: red - GT1 - Housing Cooperative „Botanik"; blue – GT2 – housing cooperative „Mikołaj Rej"; orange – GT3 – Podolsky Park; green - Zabłocie

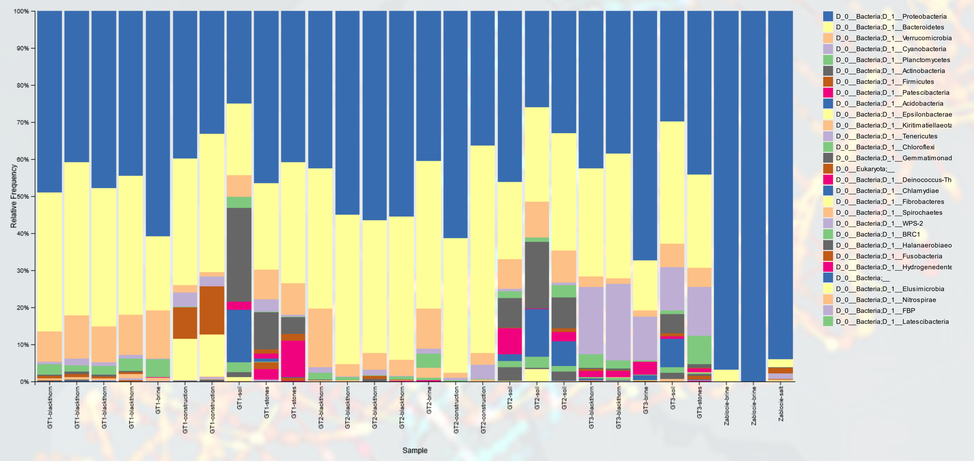


Fig.4 Taxonomic composition of the samples shown at phylum level

The biodiversity of the tested samples is presented at the phylum level in Fig. 4. It can be noticed that the samples from Zablocie are characterized by significantly lower diversity than the other samples. This is due to the much higher percentage of Protobacteria, which in the case of samples from Zablocie an average of 96.97% of the total population of microorganisms and the other samples of 44.18%. In addition, it is worth paying attention to the fact that no archaea are present in any of the samples

Fig.2 Shannon index plot shows significant difference in biodiversity between Zablocie and other groups

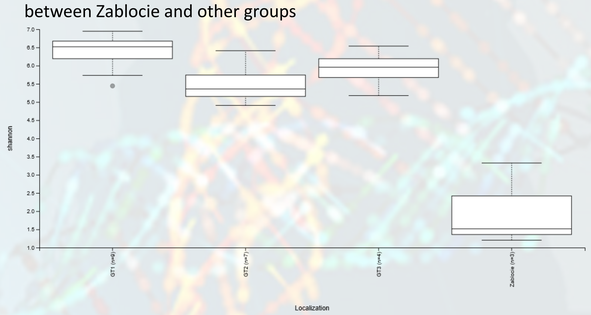
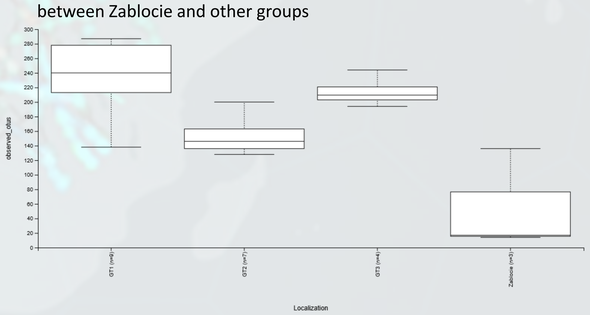


Fig. 3 Observed OTU plot shows significant difference in biodiversity between Zablocie and other groups



CONCLUSIONS

The brine from Zablocie, due to its origin from deep wells, is characterized by a low diversity of microorganisms inhabiting it. Our analysis showed that the microbiome of the graduation towers became enriched during their use as there were halophiles that were not present in the original brine used to fill graduation towers.

REFERENCES

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